

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Fuerst, Thomas R.
McAtee, C. Patrick
Yarbough, Patrice O.
Zhang, Yifan
- 10 (ii) TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Dehlinger & Associates
(B) STREET: 350 Cambridge Ave., Suite 250
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
20 (F) ZIP: 94306
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
30 (B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Fabian, Gary R.
35 (B) REGISTRATION NUMBER: 33,875
(C) REFERENCE/DOCKET NUMBER: 4600-0293.30
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (415) 324-0880
40 (B) TELEFAX: (415) 324-0960

T04610-9909260

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2049 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)
 ORF-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20 ATGCGCCCTC GGCCTATTTT GTTGCTGCTC CTCATGTTTT TGCCTATGCT GCCCGCGCCA 60
 CCGCCCGGTC AGCCGTCTGG CCGCCGTCGT GGGCGGCGCA GCGGCGGTTC CGGCGGTGGT 120
 TTCTGGGGTG ACCGGGTGTA TTCTCAGCCC TTCGCAATCC CCTATATTCA TCCAACCAAC 180
 25 CCCTTCGCCC CCGATGTCAC CGCTGCGGCC GGGGCTGGAC CTCGTGTTTC CCAACCCGCC 240
 CGACCACTCG GCTCCGCTTG GCGTGACCAG GCCCAGCGCC CCGCCGTTGC CTCACGTCGT 300
 30 AGACCTACCA CAGCTGGGGC CGCGCCGCTA ACCGCGGTTC CTCCGGCCCA TGACACCCCG 360
 CCAGTGCCTG ATGTCGACTC CCGCGGCGCC ATCTTGCGCC GGCAGTATAA CCTATCAACA 420
 TCTCCCCTTA CCTCTTCGT GGCCACCGGC ACTAACCTGG TTCTTTATGC CGCCCCTCTT 480
 35 AGTCCGCTTT TACCCCTTCA GGACGGCACC AATACCCATA TAATGGCCAC GGAAGCTTCT 540
 AATTATGCCC AGTACCGGGT TGCCCGTGCC ACAATCCGTT ACCGCCCCGCT GGTCCCCAAT 600
 40 GCTGTCGGCG GTTACGCCAT CTCCATCTCA TTCTGGCCAC AGACCACCAC CACCCCGACG 660

	TCCGTTGATA TGAATTCAAT AACCTCGACG GATGTTGCGTA TTTTAGTCCA GCCCGGCATA	720
	GCCTCTGAGC TTGTGATCCC AAGTGAGCGC CTACACTATC GTAACCAAGG CTGGCGCTCC	780
5	GTCGAGACCT CTGGGGTGGC TGAGGAGGAG GCTACCTCTG GTCTTGTTAT GCTTTGCATA	840
	CATGGCTCAC TCGTAAATTC CTATACTAAT ACACCCTATA CCGGTGCCCT CGGGCTGTTG	900
	GACTTTGCCC TTGAGCTTGA GTTTCGCAAC CTTACCCCCG GTAACACCAA TACGCGGGTC	960
10	TCCCGTTATT CCAGCACTGC TCGCCACCGC CTTCGTCGCG GTGCGGACGG GACTGCCGAG	1020
	CTCACCACCA CGGCTGCTAC CCGCTTTATG AAGGACCTCT ATTTTACTAG TACTAATGGT	1080
15	GTCGGTGAGA TCGGCCGCGG GATAGCCCTC ACCCTGTTCA ACCTTGCTGA CACTCTGCTT	1140
	GGCGGCCTGC CGACAGAATT GATTTCGTCG GCTGGTGGCC AGCTGTTCTA CTCCCGTCCC	1200
	GTTGTCTCAG CCAATGGCGA GCCGACTGTT AAGTTGTATA CATCTGTAGA GAATGCTCAG	1260
20	CAGGATAAGG GTATTGCAAT CCCGCATGAC ATTGACCTCG GAGAATCTCG TGTGGTTATT	1320
	CAGGATTATG ATAACCAACA TGAACAAGAT CGGCCGACGC CTTCTCCAGC CCCATCGCGC	1380
25	CCTTTCTCTG TCCTTCGAGC TAATGATGTG CTTTGGCTCT CTCTCACCGC TGCCGAGTAT	1440
	GACCAGTCCA CTTATGGCTC TTCGACTGGC CCAGTTTATG TTTCTGACTC TGTGACCTTG	1500
	GTTAATGTTG CGACCGGCGC GCAGGCCGTT GCCCGGTCGC TCGATTGGAC CAAGGTCACA	1560
30	CTTGACGGTC GCCCCCTCTC CACCATCCAG CAGTACTCGA AGACCTTCTT TGTCTGCCC	1620
	CTCCGCGGTA AGCTCTCTTT CTGGGAGGCA GGCACAATA AAGCCGGGTA CCCTTATAAT	1680
35	TATAACACCA CTGCTAGCGA CCAACTGCTT GTCGAGAATG CCGCCGGGCA CCGGGTCGCT	1740
	ATTTCCACTT ACACCACTAG CCTGGGTGCT GGTCCCGTCT CCATTTCTGC GGTTGCCGTT	1800
	TTAGCCCCC ACTCTGCGCT AGCATTGCTT GAGGATACCT TGGACTACCC TGCCCGCGCC	1860
40	CATACTTTTG ATGATTCTG CCCAGAGTGC CGCCCCCTTG GCCTTCAGGG CTGCGCTTTC	1920

F041210-5069260

CAGTCTACTG TCGCTGAGCT TCAGCGCCTT AAGATGAAGG TGGGTAAAAC TCGGGAGTTG 1980
 TAGTTTATTT GCTTGTGCCC CCCTTCTTTC TGTGCTTAT TTCTCATTTT TCGGTTCCGC 2040
 5 GCTCCCTGA 2049

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 2058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

20 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)
 ORF-2 region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 ATGCGCCCTA GGCCTCTTTT GCTGTTGTTT CTCTTGTTTC TGCCTATGTT GCCCGCGCCA 60
 CCGACCGGTC AGCCGTCTGG CCGCCGTCGT GGGCGGCGCA GCGGCGGTAC CGGCGGTGGT 120
 TTCTGGGGTG ACCGGGTTGA TTCTCAGCCC TTCGCAATCC CCTATATTCA TCCAACCAAC 180
 30 CCCTTTGCCC CAGACGTTGC CGCTGCGTCC GGGTCTGGAC CTCGCCTTCG CCAACCAGCC 240
 CGGCCACTTG GCTCCACTTG GCGAGATCAG GCCCAGCGCC CCTCCGCTGC CTCCCGTCGC 300
 35 CGACCTGCCA CAGCCGGGGC TCGGCGCTG ACGGCTGTGG CGCCTGCCCA TGACACCTCA 360
 CCCGTCCCGG ACGTTGATTC TCGCGGTGCA ATTCTACGCC GCCAGTATAA TTTGTCTACT 420
 TCACCCCTGA CATCCTCTGT GGCCTCTGGC ACTAATTTAG TCCTGTATGC AGCCCCCTT 480
 40 AATCCGCCTC TGCCGCTGCA GGACGGTACT AATACTCACA TTATGGCCAC AGAGGCCTCC 540

F0127-3505260

	AATTATGCAC	AGTACCGGGT	TGCCC GCGCT	ACTATCCGTT	ACCGGCCCCCT	AGTGCCTAAT	600
	GCAGTTGGAG	GCTATGCTAT	ATCCATTTCT	TTCTGGCCTC	AAACAACCAC	AACCCCTACA	660
5	TCTGTTGACA	TGAATTCCAT	TACTTCCACT	GATGTCAGGA	TTCTTGTTCA	ACCTGGCATA	720
	GCATCTGAAT	TGGTCATCCC	AAGCGAGCGC	CTTCACTACC	GCAATCAAGG	TTGGCGCTCG	780
	GTTGAGACAT	CTGGTGTTGC	TGAGGAGGAA	GCCACCTCCG	GTCTTGTCAT	GTTATGCATA	840
10	CATGGCTCTC	CAGTTAACTC	CTATACCAAT	ACCCCTTATA	CCGGTGCCCT	TGGCTTACTG	900
	GACTTTGCCT	TAGAGCTTGA	GTTTCGCAAT	CTCACCACCT	GTAACACCAA	TACACGTGTG	960
15	TCCCGTTACT	CCAGCACGGC	CCGTCACCGG	CTCCGCCGAG	GGGCCGACGG	GACTGCGGAG	1020
	CTGACCACAA	CTGCAGCCAC	CAGGTTCATG	AAAGATCTCC	ACTTTACCGG	CCTTAATGGG	1080
	GTAGGTGAAG	TCGGCCGCGG	GATAGCTCTA	ACATTACTTA	ACCTTGCTGA	CACGCTCCTC	1140
20	GGCGGGCTCC	CGACAGAATT	AATTTGTCG	GCTGGCGGGC	AACTGTTTTA	TTCCCGCCCG	1200
	GTTGTCTCAG	CCAATGGCGA	GCCAACCGTG	AAGCTCTATA	CATCAGTGGA	GAATGCTCAG	1260
	CAGGATAAGG	GTGTTGCTAT	CCCCCACGAT	ATCGATCTTG	GTGATTGCGG	TGTGGTCATT	1320
25	CAGGATTATG	ACAACCAGCA	TGAGCAGGAT	CGGCCACCC	CGTCGCCTGC	GCCATCTCGG	1380
	CCTTTTTTCTG	TTCTCCGAGC	AAATGATGTA	CTTTGGCTGT	CCCTCACTGC	AGCCGAGTAT	1440
30	GACCAGTCCA	CTTACGGGTC	GTCAACTGGC	CCGGTTTATA	TCTCGGACAG	CGTGACTTTG	1500
	GTGAATGTTG	CGACTGGCGC	GCAGGCCGTA	GCCCCGATCGC	TTGACTGGTC	CAAAGTCACC	1560
35	CTCGACGGGC	GGCCCCCTCCC	GACTGTTGAG	CAATATTCCA	AGACATTCTT	TGTGCTCCCC	1620
	CTTCGTGGCA	AGCTCTCCTT	TTGGGAGGCC	GGCACAACAA	AAGCAGGTTA	TCCTTATAAT	1680
	TATAATACTA	CTGCTAGTGA	CCAGATTCTG	ATTGAAAATG	CTGCCGGCCA	TCGGGTCGCC	1740
40	ATTTCAACCT	ATACCACCAG	GCTTGGGGCC	GGTCCGGTCG	CCATTTCTGC	GGCCGCGGTT	1800

10

15

(A) LENGTH: 1647 base pairs

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma) r62kDa,
FIGURE 2

30

35

40

	GTTCGTATTT TAGTCCAGCC CGGCATAGCC TCTGAGCTTG TGATCCCAAG TGAGCGCCTA	420
	CACTATCGTA ACCAAGGCTG GCGCTCCGTC GAGACCTCTG GGGTGGCTGA GGAGGAGGCT	480
5	ACCTCTGGTC TTGTTATGCT TTGCATACAT GGCTCACTCG TAAATTCCTA TACTAATACA	540
	CCCTATACCG GTGCCCTCGG GCTGTTGGAC TTTGCCCTTG AGCTTGAGTT TCGCAACCTT	600
10	ACCCCCGGTA ACACCAATAC GCGGGTCTCC CGTTATTCCA GCACTGCTCG CCACCGCCTT	660
	CGTCGCGGTG CGGACGGGAC TGCCGAGCTC ACCACCACGG CTGCTACCCG CTTTATGAAG	720
	GACCTCTATT TTACTAGTAC TAATGGTGTC GGTGAGATCG GCCGCGGGAT AGCCCTCACC	780
15	CTGTTCAACC TTGCTGACAC TCTGCTTGGC GGCCTGCCGA CAGAATTGAT TTCGTCGGCT	840
	GGTGGCCAGC TGTTCTACTC CCGTCCCGTT GTCTCAGCCA ATGGCGAGCC GACTGTTAAG	900
20	TTGTATACAT CTGTAGAGAA TGCTCAGCAG GATAAGGGTA TTGCAATCCC GCATGACATT	960
	GACCTCGGAG AATCTCGTGT GGTTATTCAG GATTATGATA ACCAACATGA ACAAGATCGG	1020
	CCGACGCCTT CTCCAGCCCC ATCGCGCCCT TTCTCTGTCC TTCGAGCTAA TGATGTGCTT	1080
25	TGGCTCTCTC TCACCGCTGC CGAGTATGAC CAGTCCACTT ATGGCTCTTC GACTGGCCCA	1140
	GTTTATGTTT CTGACTCTGT GACCTTGGTT AATGTTGCGA CCGGCGCGCA GGCCGTTGCC	1200
30	CGGTCGCTCG ATTGGACCAA GGTCACACTT GACGGTCGCC CCCTCTCCAC CATCCAGCAG	1260
	TACTCGAAGA CCTTCTTTGT CCTGCCGCTC CGCGGTAAGC TCTCTTTCTG GGAGGCAGGC	1320
	ACAACTAAAG CCGGGTACCC TTATAATTAT AACACCACTG CTAGCGACCA ACTGCTTGTC	1380
35	GAGAATGCCG CCGGGCACCG GGTGCTATT TCCACTTACA CCACTAGCCT GGGTGCTGGT	1440
	CCCGTCTCCA TTTCTGCGGT TGCCGTTTGA GCCCCCACT CTGCGCTAGC ATTGCTTGAG	1500
40	GATACCTTGG ACTACCCTGC CCGCGCCCAT ACTTTTGATG ATTTCTGCCC AGAGTGCCGC	1560
	CCCCTTGGCC TTCAGGGCTG CGCTTTCAG TCTACTGTCG CTGAGCTTCA GCGCCTTAAG	1620

108-99999999

ATGAAGGTGG GTAAAACTCG GGAGTTG

1647

(2) INFORMATION FOR SEQ ID NO:4:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1647 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)
 r62kDa, FIGURE 2

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGTGGCGC CTGCCCATGA CACCTCACCC GTCCCGGACG TTGATTCTCG CGGTGCAATT	60
CTACGCCGCC AGTATAATTT GTCTACTTCA CCCCTGACAT CCTCTGTGGC CTCTGGCACT	120
AATTTAGTCC TGTATGCAGC CCCCCTTAAT CCGCCTCTGC CGCTGCAGGA CGGTACTAAT	180
ACTCACATTA TGGCCACAGA GGCCTCCAAT TATGCACAGT ACCGGGTTGC CCGCGCTACT	240
ATCCGTTACC GGCCCCTAGT GCCTAATGCA GTTGGAGGCT ATGCTATATC CATTTCTTTC	300
TGGCCTCAAA CAACCACAAC CCCTACATCT GTTGACATGA ATTCCATTAC TTCCACTGAT	360
GTCAGGATTC TTGTTCAACC TGGCATAGCA TCTGAATTGG TCATCCCAAG CGAGCGCCTT	420
CACTACCGCA ATCAAGGTTG GCGCTCGGTT GAGACATCTG GTGTTGCTGA GGAGGAAGCC	480
ACCTCCGGTC TTGTCATGTT ATGCATACAT GGCTCTCCAG TTAACCTCTA TACCAATACC	540
CCTTATACCG GTGCCCTTGG CTTACTGGAC TTTGCCTTAG AGCTTGAGTT TCGCAATCTC	600
ACCACCTGTA ACACCAATAC ACGTGTGTCC CGTTACTCCA GCACGGCCCCG TCACCGGCTC	660

CGCCGAGGGG CCGACGGGAC TCGGAGCTG ACCACAAC TG CAGCCACCAG GTTCATGAAA 720

GATCTCCACT TTACCGGCCT TAATGGGGTA GGTGAAGTCG GCCGCGGGAT AGCTCTAACA 780

5 TTACTTAACC TTGCTGACAC GCTCCTCGGC GGGCTCCCGA CAGAATTAAT TTCGTCGGCT 840

GGCGGGCAAC TGTTTTATTC CCGCCCGGTT GTCTCAGCCA ATGGCGAGCC AACCGTGAAG 900

CTCTATACAT CAGTGAGAA TGCTCAGCAG GATAAGGGTG TTGCTATCCC CCACGATATC 960

10 GATCTTGGTG ATTCGCGTGT GGTCATT CAG GATTATGACA ACCAGCATGA GCAGGATCGG 1020

CCCACCCCGT CGCCTGCGCC ATCTCGGCCT TTTTCTGTTC TCCGAGCAAA TGATGTACTT 1080

15 TGGCTGTCCC TCACTGCAGC CGAGTATGAC CAGTCCACTT ACGGGTCGTC AACTGGCCCCG 1140

GTTTATATCT CGGACAGCGT GACTTTGGTG AATGTTGCGA CTGGCGCGCA GGCCGTAGCC 1200

CGATCGCTTG ACTGGTCCAA AGTCACCCTC GACGGGCGGC CCCTCCCGAC TGTTGAGCAA 1260

20 TATTCCAAGA CATTCTTTGT GCTCCCCCTT CGTGGCAAGC TCTCCTTTTG GGAGGCCGGC 1320

ACAACAAAAG CAGGTTATCC TTATAATTAT AATACTACTG CTAGTGACCA GATTCTGATT 1380

25 GAAAATGCTG CCGGCCATCG GGTCGCCATT TCAACCTATA CCACCAGGCT TGGGGCCGGT 1440

CCGGTCGCCA TTTCTGCGGC CGCGGTTTTG GCTCCACGCT CCGCCCTGGC TCTGCTGGAG 1500

GATACTTTTG ATTATCCGGG GCGGGCGCAC ACATTTGATG ACTTCTGCCC TGAATGCCGC 1560

30 GCTTTAGGCC TCCAGGGTTG TGCTTTCCAG TCAACTGTCTG CTGAGCTCCA GCGCCTTAAA 1620

GTTAAGGTGG GTAAAACTCG GGAGTTG 1647

35 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 984 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

00769066 014101

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3
region

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGC GGACG GGACTGCCGA GCTCACCACC ACGGCTGCTA CCCGCTTTAT GAAGGACCTC 60
TATTTTACTA GTACTAATGG TGTCCGTGAG ATCGGCCGCG GGATAGCCCT CACCCTGTTC 120
15 AACCTTGCTG ACACTCTGCT TGGCGGCCTG CCGACAGAAT TGATTTTCGTC GGCTGGTGGC 180
CAGCTGTTCT ACTCCCGTCC CGTTGTCTCA GCCAATGGCG AGCCGACTGT TAAGTTGTAT 240
20 ACATCTGTAG AGAATGCTCA GCAGGATAAG GGTATTGCAA TCCCGCATGA CATTGACCTC 300
GGAGAATCTC GTGTGGTTAT TCAGGATTAT GATAACCAAC ATGAACAAGA TCGGCCGACG 360
CCTTCTCCAG CCCCATCGCG CCCTTTCTCT GTCCTTCGAG CTAATGATGT GCTTTGGCTC 420
25 TCTCTCACCG CTGCCGAGTA TGACCAGTCC ACTTATGGCT CTTGCGACTGG CCCAGTTTAT 480
GTTTCTGACT CTGTGACCTT GGTTAATGTT GCGACCGGCG CGCAGGCCGT TGCCCGGTCG 540
30 CTCGATTGGA CCAAGGTCAC ACTTGACGGT CGCCCCCTCT CCACCATCCA GCAGTACTCG 600
AAGACCTTCT TTGTCCTGCC GCTCCGCGGT AAGCTCTCTT TCTGGGAGGC AGGCACAAC 660
AAAGCCGGGT ACCCTTATAA TTATAACACC ACTGCTAGCG ACCAACTGCT TGTCGAGAAT 720
35 GCCGCCGGGC ACCGGGTCGC TATTTCCACT TACACCACTA GCCTGGGTGC TGGTCCCGTC 780
TCCATTTCTG CGGTTGCCGT TTTAGCCCC CACTCTGCGC TAGCATTGCT TGAGGATACC 840
40 TTGGACTACC CTGCCGCGC CCATACTTTT GATGATTCTT GCCCAGAGTG CCGCCCCCTT 900

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 984 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain) SG3 region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGGGCCGACG	GGACTGCGGA	GCTGACCACA	ACTGCAGCCA	CCAGGTTCAT	GAAAGATCTC	60
CACTTTACCG	GCCTTAATGG	GGTAGGTGAA	GTCGGCCGCG	GGATAGCTCT	AACATTACTT	120
AACCTTGCTG	ACACGCTCCT	CGGCGGGCTC	CCGACAGAAT	TAATTTCGTC	GGCTGGCGGG	180
CAACTGTTTT	ATTCCCGCCC	GGTTGTCTCA	GCCAATGGCG	AGCCAACCGT	GAAGCTCTAT	240
ACATCAGTGG	AGAATGCTCA	GCAGGATAAG	GGTGTGCTA	TCCCCCACGA	TATCGATCTT	300
GGTGATTCGC	GTGTGGTCAT	TCAGGATTAT	GACAACCAGC	ATGAGCAGGA	TCGGCCCACC	360
CCGTCGCCTG	CGCCATCTCG	GCCTTTTTCT	GTTCTCCGAG	CAAATGATGT	ACTTTGGCTG	420
TCCCTCACTG	CAGCCGAGTA	TGACCAGTCC	ACTTACGGGT	CGTCAACTGG	CCCGGTTTAT	480
ATCTCGGACA	GCGTGAATTT	GGTGAATGTT	GCGACTGGCG	CGCAGGCCGT	AGCCCGATCG	540

CTTGACTGGT CCAAAGTCAC CCTCGACGGG CGGCCCTCC CGACTGTTGA GCAATATTCC 600

AAGACATTCT TTGTGCTCCC CCTTCGTGGC AAGCTCTCCT TTTGGGAGGC CGGCACAACA 660

5 AAAGCAGGTT ATCCTTATAA TTATAATACT ACTGCTAGTG ACCAGATTCT GATTGAAAAT 720

GCTGCCGGCC ATCGGGTCGC CATTTCACC TATACCACCA GGCTTGGGGC CGGTCCGGTC 780

10 GCCATTTCTG CGGCCGCGGT TTTGGCTCCA CGCTCCGCCC TGGCTCTGCT GGAGGATACT 840

TTTGATTATC CGGGGCGGGC GCACACATT GATGACTTCT GCCCTGAATG CCGCGCTTTA 900

GGCCTCCAGG GTTGTGCTTT CCAGTCAACT GTCGCTGAGC TCCAGCGCCT TAAAGTTAAG 960

15 GTGGGTAAAA CTCGGGAGTT GTAG 984

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)

406.3-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35 ACCTTGACT ACCCTGCCCC CGCCATACT TTTGATGATT TCTGCCAGA GTGCCGCCCC 60

CTTGGCCTTC AGGGCTGCGC TTTCCAGTCT ACTGTCGCTG AGCTTCAGCG CCTTAAGATG 120

40 AAGGTGGGTA AACTCGGGA GTTGTAG 147

F04810-9909200

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)
406.3-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTTTTGATT ATCCGGGGCG GCGCACACA TTTGATGACT TCTGCCCTGA ATGCCGCGCT 60
 TTAGGCCTCC AGGGTTGTGC TTTCCAGTCA ACTGTCGCTG AGCTCCAGCG CCTTAAAGTT 120
 AAGGTGGGTA AAACTCGGGA GTTGTAG 147

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma Strain)
ORF-3 region

F01210-530320

	ATGAATAACA	TGTCCTTTTGC	TGCGCCCATG	GGTTCGCGAC	CATGCGCCCT	CGGCCTATTT	60
5	TGTTGCTGCT	CCTCATGTTT	TTGCCTATGC	TGCCCCGCGC	ACCGCCCGGT	CAGCCGTCTG	120
	GCCGCCGTCG	TGGGCGGCGC	AGCGGCGGTT	CCGGCGGTGG	TTTCTGGGGT	GACCGGGTTG	180
10	ATTCTCAGCC	CTTCGCAATC	CCCTATATTC	ATCCAACCAA	CCCCTTCGCC	CCCGATGTCA	240
	CCGCTGCGGC	CGGGGCTGGA	CCTCGTGTTT	GCCAACCCGC	CCGACCACTC	GGCTCCGCTT	300
	GGCGTGACCA	GGCCCAGCGC	CCCGCCGTTG	CCTCACGTGC	TAGACCTACC	ACAGCTGGGG	360
15	CCGCGCCGCT	AA					372

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

30 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)
ORF-3 region

35	ATGAATAACA TGTGGTTTGC TGC GCCCATG GGTTCGCCAC CATGCGCCCT AGGCCTCTTT	60
	TGCTGTTGTT CCTCTTGTTT CTGCCTATGT TGCCCGCGCC ACCGACCGGT CAGCCGTCTG	120
40	GCCGCCGTCG TGGGCGGCGC AGCGGCGGTA CCGGCGGTGG TTTCTGGGGT GACCGGGTTG	180

ATTCTCAGCC CTTCGCAATC CCCTATATTC ATCCAACCAA CCCCTTTGCC CCAGACGTTG 240
 CCGCTGCGTC CGGGTCTGGA CCTCGCCTTC GCCAACCAGC CCGGCCACTT GGCTCCACTT 300
 5 GGCGAGATCA GGCCCAGCGC CCCTCCGCTG CCTCCCGTCG CCGACCTGCC ACAGCCGGGG 360
 CTGCGGCGCT GA 372

(2) INFORMATION FOR SEQ ID NO:11:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)
 406.4-2 region

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCAACCCGC CCGACCACTC GGCTCCGCTT GGC GTGACCA GGCCCAGCGC CCCGCCGTTG 60
 30 CCTCACGTCG TAGACCTACC ACAGCTGGGG CCGCGCCGC 99

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

0975006-0410
 101010-9909260

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)
406.4-2 region

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10 GCCAACCAGC CCGGCCACTT GGCTCCACTT GGCGAGATCA GGCCCAGCGC CCCTCCGCTG 60
CCTCCCCTCG CCGACCTGCC ACAGCCGGGG CTGCGGCGC 99

(2) INFORMATION FOR SEQ ID NO:13:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)
ORF-2

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Pro Arg Pro Ile Leu Leu Leu Leu Met Phe Leu Pro Met
1 5 10 15

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Leu Pro Ala Pro Pro Pro Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg
20 25 30

Arg Ser Gly Gly Ser Gly Gly Gly Phe Trp Gly Asp Arg Val Asp Ser
35 40 45

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Gln Pro Phe Ala Ile Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Pro

00369066-0424
F01240-9909200

	50		55		60
	Asp Val Thr Ala Ala Ala Gly Ala Gly Pro Arg Val Arg Gln Pro Ala				
	65		70		75 80
5	Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ala Gln Arg Pro Ala Val				
		85		90	95
	Ala Ser Arg Arg Arg Pro Thr Thr Ala Gly Ala Ala Pro Leu Thr Ala				
10		100		105	110
	Val Ala Pro Ala His Asp Thr Pro Pro Val Pro Asp Val Asp Ser Arg				
		115		120	125
15	Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr				
		130		135	140
	Ser Ser Val Ala Thr Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu				
	145		150		155 160
20	Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala				
		165		170	175
	Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr Ile				
25		180		185	190
	Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser				
		195		200	205
30	Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met				
		210		215	220
	Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile				
	225		230		235 240
35	Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln				
		245		250	255
	Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala Thr				
40		260		265	270

009006-0404
009006-0404

	Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Leu Val Asn Ser Tyr	
	275	280 285
5	Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu	
	290	295 300
	Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg Val	
	305	310 315 320
10	Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp	
		325 330 335
	Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp	
		340 345 350
15	Leu Tyr Phe Thr Ser Thr Asn Gly Val Gly Glu Ile Gly Arg Gly Ile	
		355 360 365
	Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro	
20		370 375 380
	Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro	
		385 390 395 400
25	Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val	
		405 410 415
	Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp	
		420 425 430
30	Leu Gly Glu Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu	
		435 440 445
	Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val	
35		450 455 460
	Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr	
		465 470 475 480
40	Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Val Ser Asp	
		485 490 495

F010210-99069260

	Ser	Leu	Asp	Trp	Thr	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Ser	Thr
5			515					520					525			

10 Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn
 545 550 555 560

15
His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro
580 585 590

Leu Leu Glu Asp Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe Asp
610 615 620

Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys
645 650 655

(2) INFORMATION FOR SEQ ID NO:14:

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(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

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Asn Pro Pro Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala
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Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr Ile
 180 185 190

5 Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser
 195 200 205

Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met
 210 215 220

10 Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile
 225 230 235 240

Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln
 245 250 255

15 Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala Thr
 260 265 270

20 Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr
 275 280 285

Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu
 290 295 300

25 Glu Leu Glu Phe Arg Asn Leu Thr Thr Cys Asn Thr Asn Thr Arg Val
 305 310 315 320

Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp
 325 330 335

30 Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp
 340 345 350

35 Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly Arg Gly Ile
 355 360 365

Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro
 370 375 380

40 Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro
 385 390 395 400

0025006-01244

Residue	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val				
						405					410					415				
5																				
	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Val	Ala	Ile	Pro	His	Asp	Ile	Asp				
				420					425					430						
	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His	Glu				
			435					440					445							
10																				
	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	Val				
		450					455					460								
	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	Tyr				
	465					470				475						480				
15																				
	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr	Ile	Ser	Asp				
					485					490					495					
20																				
	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	Arg				
				500					505					510						
	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Pro	Thr				
			515					520					525							
25																				
	Val	Glu	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly	Lys				
		530					535					540								
	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr	Asn				
	545					550														

Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Val Lys Val Gly Lys
645 650 655

10 (2) INFORMATION FOR SEQ ID NO:15:

(A) LENGTH: 549 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain)
r62kDa, FIGURE 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Val Ala Pro Ala His Asp Thr Pro Pro Val Pro Asp Val Asp Ser
1 5 10 15

Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu
20 25 30

Thr Ser Ser Val Ala Thr Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro
35 40 45

Leu Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met
50 55 60

Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr

	65		70		75		80									
	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile
						85				90					95	
5	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp
						100				105				110		
	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly
10			115					120						125		
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn
		130						135						140		
15	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala
	145					150					155				160	
	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Leu	Val	Asn	Ser
						165				170					175	
20	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala
						180				185				190		
	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg
25			195					200					205			
	Val	Ser	Arg	Tyr	Ser	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala
		210						215				220				
30	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys
	225					230					235				240	
	Asp	Leu	Tyr	Phe	Thr	Ser	Thr	Asn	Gly	Val	Gly	Glu	Ile	Gly	Arg	Gly
						245				250				255		
35	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu
						260				265				270		
	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg
40						275				280			285			

TOH210: 9909220

	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser
	290						295						300			
5	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His	Asp	Ile
	305					310					315					320
	Asp	Leu	Gly	Glu	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His
					325					330					335	
10	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser
					340					345				350		
	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu
					355				360				365			
15	Tyr	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr	Val	Ser
		370					375					380				
	Asp	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala
20		385				390					395					400
	Arg	Ser	Leu	Asp	Trp	Thr	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Ser
					405					410					415	
25	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly
					420				425					430		
	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr
					435			440					445			
30	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Leu	Leu	Val	Glu	Asn	Ala	Ala
		450					455					460				
	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly	Ala	Gly
35		465				470					475					480
	Pro	Val	Ser	Ile	Ser	Ala	Val	Ala	Val	Leu	Ala	Pro	His	Ser	Ala	Leu
					485					490					495	
40	Ala	Leu	Leu	Glu	Asp	Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe
					500				505					510		

Asp Asp Phe Cys Pro Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala
515 520 525

5 Phe Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Met Lys Val Gly
530 535 540

Lys Thr Arg Glu Leu
545

10 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 549 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

20 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

- 25 (C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)
r62kDa, FIGURE 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

30 Ala Val Ala Pro Ala His Asp Thr Ser Pro Val Pro Asp Val Asp Ser
1 5 10 15

Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu
20 25 30

35 Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro
35 40 45

Leu Asn Pro Pro Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met
50 55 60

40 Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr

0096006-4114

	65					70						75					80
	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	
					85					90					95		
5																	
	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	
				100					105					110			
10	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	
			115					120					125				
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	
		130					135					140					
15	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala	
	145					150					155					160	
	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	
				165						170					175		
20																	
	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	
			180						185					190			
	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Thr	Cys	Asn	Thr	Asn	Thr	Arg	
25			195					200					205				
	Val	Ser	Arg	Tyr	Ser	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	
		210					215					220					
30	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	
	225					230					235					240	
	Asp	Leu	His	Phe	Thr	Gly	Leu	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	
				245						250					255		
35																	
	Ile	Ala	Leu	Thr	Leu	Leu	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	
			260						265					270			
	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	
40			275					280					285				

Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser
290 295 300

5 Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His Asp Ile
305 310 315 320

Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His
325 330 335

10 Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser
340 345 350

Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu
355 360 365

15 Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Ile Ser
370 375 380

20 Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala
385 390 395 400

Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Pro
405 410 415

25 Thr Val Glu Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg Gly
420 425 430

Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr
435 440 445

30 Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala
450 455 460

35 Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Arg Leu Gly Ala Gly
465 470 475 480

Pro Val Ala Ile Ser Ala Ala Ala Val Leu Ala Pro Arg Ser Ala Leu
485 490 495

40 Ala Leu Leu Glu Asp Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe
500 505 510

00960065-01404
T01210-9909260

	Thr	Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His
					85					90					95	
5	Asp	Ile	Asp	Leu	Gly	Glu	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn
	100								105					110		
	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro
	115				120				125							
10	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala
	130				135				140							
	Ala	Glu	Tyr	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr
	145				150				155				160			
15	Val	Ser	Asp	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala
	165				170				175							
20	Val	Ala	Arg	Ser	Leu	Asp	Trp	Thr	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro
	180				185				190							
	Leu	Ser	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu
	195				200				205							
25	Arg	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr
	210				215				220							
	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Leu	Leu	Val	Glu	Asn
	225				230				235				240			
30	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly
	245				250				255							
	Ala	Gly	Pro	Val	Ser	Ile	Ser	Ala	Val	Ala	Val	Leu	Ala	Pro	His	Ser
35	260				265				270							
	Ala	Leu	Ala	Leu	Leu	Glu	Asp	Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His
	275				280				285							
40	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Pro	Leu	Gly	Leu	Gln	Gly
	290				295				300							

Cys Ala Phe Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Met Lys
 305 310 315 320

Val Gly Lys Thr Arg Glu Leu
 325

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

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- (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)
 SG3 region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

25

Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe
 1 5 10 15

Met Lys Asp Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly
 20 25 30

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Arg Gly Ile Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly
 35 40 45

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Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr
 50 55 60

Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr
 65 70 75 80

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Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His
 85 90 95

000000-99009260

	Asp Ile Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn
	100 105 110
5	Gln His Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro
	115 120 125
	Phe Ser Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala
	130 135 140
10	Ala Glu Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr
	145 150 155 160
	Ile Ser Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala
	165 170 175
15	Val Ala Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro
	180 185 190
	Leu Pro Thr Val Glu Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu
20	195 200 205
	Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr
	210 215 220
25	Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn
	225 230 235 240
	Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Arg Leu Gly
	245 250 255
30	Ala Gly Pro Val Ala Ile Ser Ala Ala Ala Val Leu Ala Pro Arg Ser
	260 265 270
	Ala Leu Ala Leu Leu Glu Asp Thr Phe Asp Tyr Pro Gly Arg Ala His
35	275 280 285
	Thr Phe Asp Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly
	290 295 300
40	Cys Ala Phe Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Val Lys
	305 310 315 320

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Val Gly Lys Thr Arg Glu Leu
325

(2) INFORMATION FOR SEQ ID NO:19:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

15

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)
406.4-2

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala Asn Pro Pro Asp His Ser Ala Pro Leu Gly Val Thr Arg Pro Ser
1 5 10 15

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Ala Pro Pro Leu Pro His Val Val Asp Leu Pro Gln Leu Gly Pro Arg
 20 25 30

Arg

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: protein

40

(iii) HYPOTHETICAL: NO

0076906-0434

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)
406.4-2

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser
1 5 10 15

10

Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu Arg
20 25 30

Arg

15

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 124 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

25

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma Strain)
ORF-3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

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Met Asn Asn Met Ser Phe Ala Ala Pro Met Gly Ser Arg Pro Cys Ala
1 5 10 15

Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro
20 25 30

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Arg His Arg Pro Val Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala

F01110-9909260

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Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro
 50 55 60

5

Ser Gln Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser
 65 70 75 80

10

Pro Leu Arg Pro Gly Leu Asp Leu Val Phe Ala Asn Pro Pro Asp His
 85 90 95

Ser Ala Pro Leu Gly Val Thr Arg Pro Ser Ala Pro Pro Leu Pro His
 100 105 110

15

Val Val Asp Leu Pro Gln Leu Gly Pro Arg Arg Glx
 115 120

(2) INFORMATION FOR SEQ ID NO:22:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

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- (vi) ORIGINAL SOURCE:
 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)
 ORF-3

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Asn Asn Met Trp Phe Ala Ala Pro Met Gly Ser Pro Pro Cys Ala
 1 5 10 15

40

Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro
 20 25 30

10111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001301130213031304130513061307130813091310131113121313131413151316131713181319132013211322132313241325132613271328132913301331133213331334133513361337133813391340134113421343134413451346134713481349135013511352135313541355135613571358135913601361136213631364136513661367136813691370137113721373137413751376137713781379138013811382138313841385138613871388138913901391139213931394139513961397139813991400140114021403140414051406140714081409141014111412141314141415141614171418141914201421142214231424142514261427142814291430143114321433143414351436143714381439144014411442144314441445144614471448144914501451145214531454145514561457145814591460146114621463146414651466146714681469147014711472147314741475147614771478147914801481148214831484148514861487148814891490149114921493149414951496149714981499150015011502150315041505150615071508150915101511151215131514151515161517151815191520152115221523152415251526152715281529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27802781278227832784278527862787278827892790279127922793279427952796279727982799280028012802280328042805280628072808280928102811281228132814281528162817281828192820282128222823282428252826282728282829283028312832283328342835283628372838283928402841284228432844284528462847284828492850285128522853285428552856285728582859286028612862286328642865286628672868286928702871287228732874287528762877287828792880288128822883288428852886288728882889289028912892289328942895289628972898289929002901290229032904290529062907290829092910291129122913291429152916291729182919292029212922292329242925292629272928292929302931293229332934293529362937293829392940294129422943294429452946294729482949295029512952295329542955295629572958295929602961296229632964296529662967296829692970297129722973297429752976297729782979298029812982298329842985298629872988298929902991299229932994299529962997299829993000300130023003300430053006300730083009301030113012301330143015301630173018301930203021302230233024302530263027302830293030303130323033303430353036303730383039304030413042304330443045304630473048304930503051305230533054305530563057305830593060306130

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(iii) HYPOTHETICAL: NO

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(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)
406.3-2

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Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val
20 25 30

5 (2) INFORMATION FOR SEQ ID NO:24:

10 (D) TOPOLOGY: linear

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(vi) ORIGINAL SOURCE:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

25
Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val
20 25 30

Ala Glu Leu Gln Arg Leu Lys Val Lys Val Gly Lys Thr Arg Glu Leu
30 35 40 45

(2) INFORMATION FOR SEQ ID NO:25:

35 (A) LENGTH: 540 amino acids

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain)

5 r62kDa, 58.1 kDa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

10 Ala Val Ala Pro Ala His Asp Thr Pro Pro Val Pro Asp Val Asp Ser
1 5 10 15

Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu
20 25 30

15 Thr Ser Ser Val Ala Thr Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro
35 40 45

Leu Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met
20 50 55 60

Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr
65 70 75 80

25 Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile
85 90 95

Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp
100 105 110

30 Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly
115 120 125

Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn
35 130 135 140

Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala
145 150 155 160

40 Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Leu Val Asn Ser
165 170 175

101-9909260

[illegible]

	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly
5				420					425					430		

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10      Asn Tyr Asn Thr  Thr Ala  Ser Asp Gln Leu Leu Val Glu Asn Ala Ala
          450                      455                      460

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Pro Val Ser Ile Ser Ala Val Ala Val Leu Ala Pro His Ser Ala Leu

485 490 495

Asp Asp Phe Cys Pro Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala
515 520 525

(2) INFORMATION FOR SEQ ID NO:26:

35

(ii) MOLECULE TYPE: protein

40 (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)

5		Ala Val Ala Pro Ala His Asp Thr Ser Pro Val Pro Asp Val Asp Ser	
	1	5	10 15
	Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu		
	20	25	30
10	Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro		
	35	40	45
	Leu Asn Pro Pro Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met		
15	50	55	60
	Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr		
	65	70	75 80
20	Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile		
	85	90	95
	Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp		
	100	105	110
25	Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly		
	115	120	125
	Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn		
30	130	135	140
	Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala		
	145	150	155 160
35	Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn Ser		
	165	170	175
	Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala		
	180	185	190
40	Leu Glu Leu Glu Phe Arg Asn Leu Thr Thr Cys Asn Thr Asn Thr Arg		

195

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205

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Val Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala
210 215 220

Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys
225 230 235 240

10

Asp Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly Arg Gly
245 250 255

Ile Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu
260 265 270

15

Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg
275 280 285

Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser
290 295 300

20

Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His Asp Ile
305 310 315 320

Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His
325 330 335

25

Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser
340 345 350

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Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu
355 360 365

Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Ile Ser
370 375 380

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Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala
385 390 395 400

Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Pro
405 410 415

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101210-33065260

Thr Val Glu Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg Gly
420 425 430

5 Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr
435 440 445

Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala
450 455 460

10 Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Arg Leu Gly Ala Gly
465 470 475 480

Pro Val Ala Ile Ser Ala Ala Ala Val Leu Ala Pro Arg Ser Ala Leu
485 490 495

15 Ala Leu Leu Glu Asp Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe
500 505 510

20 Asp Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala
515 520 525

Phe Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys
530 535 540

25 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 525 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain)
r62kDa, 56.5 kDa

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144-999999999

	Ala	Val	Ala	Pro	Ala	His	Asp	Thr	Pro	Pro	Val	Pro	Asp	Val	Asp	Ser	
	1					5					10					15	
5																	
	Arg	Gly	Ala	Ile	Leu	Arg	Arg	Gln	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Leu	
				20					25					30			
	Thr	Ser	Ser	Val	Ala	Thr	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	
10			35					40						45			
	Leu	Ser	Pro	Leu	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	
		50					55					60					
15	Ala	Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Ala	Arg	Ala	Thr	
	65					70					75					80	
	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	
					85					90					95		
20																	
	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	
				100					105					110			
	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	
25			115					120					125				
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	
		130					135					140					
30	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala	
	145					150					155					160	
	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Leu	Val	Asn	Ser	
				165						170					175		
35																	
	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	
				180					185					190			
	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	
40			195					200					205				

	Val	Ser	Arg	Tyr	Ser	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	
	210						215					220					
5	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	
	225					230				235						240	
	Asp	Leu	Tyr	Phe	Thr	Ser	Thr	Asn	Gly	Val	Gly	Glu	Ile	Gly	Arg	Gly	
					245				250						255		
10	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	
				260					265					270			
	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	
		275						280					285				
15	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	
		290					295					300					
	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His	Asp	Ile	
20	305					310					315					320	
	Asp	Leu	Gly	Glu	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His	
					325				330					335			
25	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	
				340				345					350				
	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	
		355					360					365					
30	Tyr	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr	Val	Ser	
	370						375					380					
	Asp	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	
35	385					390				395						400	
	Arg	Ser	Leu	Asp	Trp	Thr	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Ser	
				405					410				415				
40	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly	
				420				425				430					

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Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr
435 440 445

5 Asn Tyr Asn Thr Thr Ala Ser Asp Gln Leu Leu Val Glu Asn Ala Ala
450 455 460

Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly
465 470 475 480

10 Pro Val Ser Ile Ser Ala Val Ala Val Leu Ala Pro His Ser Ala Leu
485 490 495

Ala Leu Leu Glu Asp Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe
500 505 510

15 Asp Asp Phe Cys Pro Glu Cys Arg Pro Leu Gly Leu Gln
515 520 525

(2) INFORMATION FOR SEQ ID NO:28:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 525 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30 (vi) ORIGINAL SOURCE:
(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)
r62kDa, 56.5 kDa

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
Ala Val Ala Pro Ala His Asp Thr Ser Pro Val Pro Asp Val Asp Ser
1 5 10 15

40 Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu
20 25 30

09769066-0400

	Thr	Ser	Ser	Val	Ala	Ser	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	
				35					40								45
5	Leu	Asn	Pro	Pro	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	
		50					55					60					
	Ala	Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Ala	Arg	Ala	Thr	
	65					70					75					80	
10	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	
					85						90				95		
	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	
				100					105					110			
15	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	
			115					120					125				
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	
20		130					135					140					
	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala	
	145					150					155					160	
25	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	
				165						170					175		
	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	
				180					185					190			
30	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Thr	Cys	Asn	Thr	Asn	Thr	Arg	
		195						200					205				
	Val	Ser	Arg	Tyr	Ser	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	
35		210					215					220					
	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	
	225					230					235					240	
40	Asp	Leu	His	Phe	Thr	Gly	Leu	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	
					245					250						255	

5	Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg	275	280	285
	Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser	290	295	300
10	Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His Asp Ile	305	310	315
	Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His	325	330	335
15	Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser	340	345	350
	Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu	355	360	365
20	Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Ile Ser	370	375	380
	Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala	385	390	395
25	Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Pro	405	410	415
30	Thr Val Glu Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg Gly	420	425	430
	Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr	435	440	445
35	Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala	450	455	460
40	Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Arg Leu Gly Ala Gly	465	470	475
				480

Ala Leu Leu Glu Asp Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe
500 505 510

10 (2) INFORMATION FOR SEQ ID NO:29:

(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (iii) HYPOTHETICAL: NO

(C) INDIVIDUAL ISOLATE: HEV 5' primer

GGGGGGGATC CATATGGCGG TCGCTCCGGC CCATGACACC CCG

43

(2) INFORMATION FOR SEQ ID NO:30:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(C) INDIVIDUAL ISOLATE: HEV 3' primer

ATTAGAAGCT TCCGTGGCCA TTATATG

27

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Modified-site

(B) LOCATION: 3

(D) OTHER INFORMATION: /note= "where Xaa is Q or P"

```

35      (ix) FEATURE:
          (A) NAME/KEY: Modified-site
          (B) LOCATION: 5
          (D) OTHER INFORMATION: /note= "where Xaa is G or D"

```

```

      (ix) FEATURE:
      (A) NAME/KEY: Modified-site
40      (B) LOCATION: 7
      (D) OTHER INFORMATION: /note= "where Xaa is L or S"

```

5

- (ix) FEATURE:

- 10

15

- (ix) **FEATURE:**

- 20

(ix) FEATURE:

- 25

(ix) **FEATURE:**

- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

35

40

Arg